

OIPE

## RAW SEQUENCE LISTING

DATE: 08/13/2001

PATENT APPLICATION: US/09/920,677

TIME: 11:07:29

Input Set : A:\RTS-0245 Sequence Listing.txt

Output Set: N:\CRF3\08132001\I920677.raw

Does Not Comply  
Corrected Diskette Needed

```

6 <110> APPLICANT: Brett P. Monia
7   Lex M. Cowsert
9 <120> TITLE OF INVENTION: ANTISENSE MODULATION OF P70 S6 KINASE EXPRESSION
11 <130> FILE REFERENCE: RTS-0245
C--> 13 <140> CURRENT APPLICATION NUMBER: US/09/920,677
C--> 13 <141> CURRENT FILING DATE: 2001-08-01
13 <160> NUMBER OF SEQ ID NOS: 49
16 <210> SEQ ID NO: 1
17 <211> LENGTH: 20
18 <212> TYPE: DNA
19 <213> ORGANISM: Artificial Sequence
21 <220> FEATURE:
23 <223> OTHER INFORMATION: Antisense Oligonucleotide
25 <400> SEQUENCE: 1
26 tccgtcatcg ctccctcaggg                                     20
29 <210> SEQ ID NO: 2
30 <211> LENGTH: 20
31 <212> TYPE: DNA
32 <213> ORGANISM: Artificial Sequence
34 <220> FEATURE:
36 <223> OTHER INFORMATION: Antisense Oligonucleotide
38 <400> SEQUENCE: 2
39 atgcattctg cccccaagga                                     20
42 <210> SEQ ID NO: 3
43 <211> LENGTH: 2346
44 <212> TYPE: DNA
45 <213> ORGANISM: Homo sapiens
47 <220> FEATURE:
49 <220> FEATURE:
50 <221> NAME/KEY: CDS
51 <222> LOCATION: (28)...(1605)
53 <400> SEQUENCE: 3
54 gcacgaggct gcggcgggtc cgggccc atg agg cga cga agg agg cgg gac ggc       54
55                               Met Arg Arg Arg Arg Arg Arg Arg Asp Gly
56                               1           5
58 ttt tac cca gcc ccg gac ttc cga gac agg gaa gct gag gac atg gca       102
59 Phe Tyr Pro Ala Pro Asp Phe Arg Asp Arg Glu Ala Glu Asp Met Ala
60 10           15           20           25
62 gga gtg ttt gac ata gac ctg gac cag cca gag gac gcg ggc tct gag       150
63 Gly Val Phe Asp Ile Asp Leu Asp Gln Pro Glu Asp Ala Gly Ser Glu
64           30           35           40
66 gat gag ctg gag gag ggg ggt cag tta aat gaa agc atg gac cat ggg       198
67 Asp Glu Leu Glu Glu Gly Gly Gln Leu Asn Glu Ser Met Asp His Gly
68           45           50           55
70 gga gtt gga cca tat gaa ctt ggc atg gaa cat tgt gag aaa ttt gaa       246
71 Gly Val Gly Pro Tyr Glu Leu Gly Met Glu His Cys Glu Lys Phe Glu
72           60           65           70

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74	atc tca gaa act agt gtg aac aga ggg cca gaa aaa atc aga cca gaa	294
75	Ile Ser Glu Thr Ser Val Asn Arg Gly Pro Glu Lys Ile Arg Pro Glu	
76	75 80 85	
78	tgt ttt gag cta ctt cgg gta ctt ggt aaa ggg ggc tat gga aag gtt	342
79	Cys Phe Glu Leu Leu Arg Val Leu Gly Lys Gly Gly Tyr Gly Lys Val	
80	90 95 100 105	
82	ttt caa gta cga aaa gta aca gga gca aat act ggg aaa ata ttt gcc	390
83	Phe Gln Val Arg Lys Val Thr Gly Ala Asn Thr Gly Lys Ile Phe Ala	
84	110 115 120	
86	atg aag gtg ctt aaa aag gca atg ata gta aga aat gct aaa gat aca	438
87	Met Lys Val Leu Lys Lys Ala Met Ile Val Arg Asn Ala Lys Asp Thr	
88	125 130 135	
90	gct cat aca aaa gca gaa cgg aat att ctg gag gaa gta aag cat ccc	486
91	Ala His Thr Lys Ala Glu Arg Asn Ile Leu Glu Glu Val Lys His Pro	
92	140 145 150	
94	ttc atc gtg gat tta att tat gcc ttt cag act ggt gga aaa ctc tac	534
95	Phe Ile Val Asp Leu Ile Tyr Ala Phe Gln Thr Gly Gly Lys Leu Tyr	
96	155 160 165	
98	ctc atc ctt gag tat ctc agt gga gga gaa cta ttt atg cag tta gaa	582
99	Leu Ile Leu Glu Tyr Leu Ser Gly Gly Glu Leu Phe Met Gln Leu Glu	
100	170 175 180 185	
102	aga gag gga ata ttt atg gaa gac act gcc tgc ttt tac ttg gca gaa	630
103	Arg Glu Gly Ile Phe Met Glu Asp Thr Ala Cys Phe Tyr Leu Ala Glu	
104	190 195 200	
106	atc tcc atg gct ttg ggg cat tta cat caa aag ggg atc atc tac aga	678
107	Ile Ser Met Ala Leu Gly His Leu His Gln Lys Gly Ile Ile Tyr Arg	
108	205 210 215	
110	gac ctg aag ccg gag aat atc atg ctt aat cac caa ggt cat gtg aaa	726
111	Asp Leu Lys Pro Glu Asn Ile Met Leu Asn His Gln Gly His Val Lys	
112	220 225 230	
114	cta aca gac ttt gga cta tgc aaa gaa tct att cat gat gga aca gtc	774
115	Leu Thr Asp Phe Gly Leu Cys Lys Glu Ser Ile His Asp Gly Thr Val	
116	235 240 245	
118	aca cac aca ttt tgt gga aca ata gaa tac atg gcc cct gaa atc ttg	822
119	Thr His Thr Phe Cys Gly Thr Ile Glu Tyr Met Ala Pro Glu Ile Leu	
120	250 255 260 265	
122	atg aga agt ggc cac aat cgt gct gtg gat tgg tgg agt ttg gga gca	870
123	Met Arg Ser Gly His Asn Arg Ala Val Asp Trp Trp Ser Leu Gly Ala	
124	270 275 280	
126	tta atg tat gac atg ctg act gga gca ccc cca ttc act ggg gag aat	918
127	Leu Met Tyr Asp Met Leu Thr Gly Ala Pro Pro Phe Thr Gly Glu Asn	
128	285 290 295	
130	aga aag aaa aca att gac aaa atc ctc aaa tgt aaa ctc aat ttg cct	966
131	Arg Lys Lys Thr Ile Asp Lys Ile Leu Lys Cys Lys Leu Asn Leu Pro	
132	300 305 310	
134	ccc tac ctc aca caa gaa gcc aga gat ctg ctt aaa aag ctg ctg aaa	1014
135	Pro Tyr Leu Thr Gln Glu Ala Arg Asp Leu Leu Lys Lys Leu Leu Lys	
136	315 320 325	
138	aga aat gct gct tct cgt ctg gga gct ggt cct ggg gac gct gga gaa	1062

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139	Arg	Asn	Ala	Ala	Ser	Arg	Leu	Gly	Ala	Gly	Pro	Gly	Asp	Ala	Gly	Glu	
140	330					335					340					345	
142	gtt	caa	gct	cat	cca	ttc	ttt	aga	cac	att	aac	tgg	gaa	gaa	ctt	ctg	1110
143	Val	Gln	Ala	His	Pro	Phe	Phe	Arg	His	Ile	Asn	Trp	Glu	Glu	Leu	Leu	
144					350					355					360		
146	gct	cga	aag	gtg	gag	ccc	ccc	ttt	aaa	cct	ctg	ttg	caa	tct	gaa	gag	1158
147	Ala	Arg	Lys	Val	Glu	Pro	Pro	Phe	Lys	Pro	Leu	Leu	Gln	Ser	Glu	Glu	
148					365					370					375		
150	gat	gta	agt	cag	ttt	gat	tcc	aag	ttt	aca	cgt	cag	aca	cct	gtc	gac	1206
151	Asp	Val	Ser	Gln	Phe	Asp	Ser	Lys	Phe	Thr	Arg	Gln	Thr	Pro	Val	Asp	
152					380					385					390		
154	agc	cca	gat	gac	tca	act	ctc	agt	gaa	agt	gcc	aat	cag	gtc	ttt	ctg	1254
155	Ser	Pro	Asp	Asp	Ser	Thr	Leu	Ser	Glu	Ser	Ala	Asn	Gln	Val	Phe	Leu	
156					395					400					405		
158	ggg	ttt	aca	tat	gtg	gct	cca	tct	gta	ctt	gaa	agt	gtg	aaa	gaa	aag	1302
159	Gly	Phe	Thr	Tyr	Val	Ala	Pro	Ser	Val	Leu	Glu	Ser	Val	Lys	Glu	Lys	
160	410					415					420				425		
162	ttt	tcc	ttt	gaa	cca	aaa	atc	cga	tca	cct	cga	aga	ttt	att	ggc	agc	1350
163	Phe	Ser	Phe	Glu	Pro	Lys	Ile	Arg	Ser	Pro	Arg	Arg	Phe	Ile	Gly	Ser	
164					430					435					440		
166	cca	cga	aca	cct	gtc	agc	cca	gtc	aaa	ttt	tct	cct	ggg	gat	ttc	tgg	1398
167	Pro	Arg	Thr	Pro	Val	Ser	Pro	Val	Lys	Phe	Ser	Pro	Gly	Asp	Phe	Trp	
168					445					450					455		
170	gga	aga	ggg	gct	tcg	gcc	agc	aca	gca	aat	cct	cag	aca	cct	gtg	gaa	1446
171	Gly	Arg	Gly	Ala	Ser	Ala	Ser	Thr	Ala	Asn	Pro	Gln	Thr	Pro	Val	Glu	
172					460					465					470		
174	tac	cca	atg	gaa	aca	agt	ggc	ata	gag	cag	atg	gat	gtg	aca	atg	agt	1494
175	Tyr	Pro	Met	Glu	Thr	Ser	Gly	Ile	Glu	Gln	Met	Asp	Val	Thr	Met	Ser	
176					475					480					485		
178	ggg	gaa	gca	tcg	gca	cca	ctt	cca	ata	cga	cag	ccg	aac	tct	ggg	cca	1542
179	Gly	Glu	Ala	Ser	Ala	Pro	Leu	Pro	Ile	Arg	Gln	Pro	Asn	Ser	Gly	Pro	
180	490					495					500				505		
182	tac	aaa	aaa	caa	gct	ttt	ccc	atg	atc	tcc	aaa	cgg	cca	gag	cac	ctg	1590
183	Tyr	Lys	Lys	Gln	Ala	Phe	Pro	Met	Ile	Ser	Lys	Arg	Pro	Glu	His	Leu	
184					510					515					520		
186	cgt	atg	aat	cta	tga	cagagcaatg	cttttaatga	atttaaggca	aaaagggtgga								1645
187	Arg	Met	Asn	Leu													
188					525												
190	gagggagatg	tgtgagcattc	ctgcaagggtg	aaacaagact	caaaatgaca	gtttcagaga											1705
192	gtcaatgtca	ttacatagaa	cacttcggac	acaggaaaaa	taaacgtgga	ttttaaaaaa											1765
194	tcaatcaatg	gtgcaaaaaa	aaacttaaaag	caaaatagta	ttgctgaact	cttaggcaca											1825
196	tcaattaatt	gattcctcgc	gacatctttc	tcaaccttat	caaggatttt	catgttgatg											1885
198	actcgaaact	gacagtatta	agggtaggat	gttgctctga	atcactgtga	gtctgatgtg											1945
200	tgaagaagg	tatcctttca	ttaggcaagt	acaaattgcc	tataataactt	gcaactaagg											2005
202	acaaattagc	atgcaagctt	ggtcaaaactt	ttcccaggca	aatggggaag	gcaaagacaa											2065
204	aagaaactta	ccaattgatg	ttttacgtgc	aaacaacctg	aatctttttt	ttatataaat											2125
206	atatattttt	caaatagatt	tttgattcag	ctcattatga	aaaacatccc	aaacttttaa											2185
208	atgcgaaatt	attgggttgg	gtgaagaaag	ccagacaact	tctgtttctt	ctcttggtga											2245
210	aataataaaa	tgcaaatgaa	tcattgttaa	cacagctgtg	gctcgtttga	gggattgggg											2305

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212 tggacctggg gtttattttc agtaaccacg ctgcggagcc t 2346
215 <210> SEQ ID NO: 4
216 <211> LENGTH: 24
217 <212> TYPE: DNA
218 <213> ORGANISM: Artificial Sequence
220 <220> FEATURE:
222 <223> OTHER INFORMATION: PCR Primer
224 <400> SEQUENCE: 4
225 attgctgaac tcttaggcac atca 24
228 <210> SEQ ID NO: 5
229 <211> LENGTH: 24
230 <212> TYPE: DNA
231 <213> ORGANISM: Artificial Sequence
233 <220> FEATURE:
235 <223> OTHER INFORMATION: PCR Primer
237 <400> SEQUENCE: 5
238 tgtcagtttc gagtcatcaa catg 24
241 <210> SEQ ID NO: 6
242 <211> LENGTH: 32
243 <212> TYPE: DNA
244 <213> ORGANISM: Artificial Sequence
246 <220> FEATURE:
248 <223> OTHER INFORMATION: PCR Probe
250 <400> SEQUENCE: 6
251 ctgcgcacat ctttctcaac cttatcaagg at 32
254 <210> SEQ ID NO: 7
255 <211> LENGTH: 19
256 <212> TYPE: DNA
257 <213> ORGANISM: Artificial Sequence
259 <220> FEATURE:
261 <223> OTHER INFORMATION: PCR Primer
263 <400> SEQUENCE: 7
264 gaaggtgaag gtcggagtc 19
267 <210> SEQ ID NO: 8
268 <211> LENGTH: 20
269 <212> TYPE: DNA
270 <213> ORGANISM: Artificial Sequence
272 <220> FEATURE:
274 <223> OTHER INFORMATION: PCR Primer
276 <400> SEQUENCE: 8
277 gaagatggtg atgggatttc 20
280 <210> SEQ ID NO: 9
281 <211> LENGTH: 20
282 <212> TYPE: DNA
283 <213> ORGANISM: Artificial Sequence
285 <220> FEATURE:
287 <223> OTHER INFORMATION: PCR Probe
289 <400> SEQUENCE: 9
290 caagcttccc gttctcagcc 20

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293 <210> SEQ ID NO: 10
294 <211> LENGTH: 20
295 <212> TYPE: DNA
296 <213> ORGANISM: Artificial Sequence
298 <220> FEATURE:
300 <223> OTHER INFORMATION: Antisense Oligonucleotide
302 <400> SEQUENCE: 10
303 ggacccgccg cagcctcgtg 20
306 <210> SEQ ID NO: 11
307 <211> LENGTH: 20
308 <212> TYPE: DNA
309 <213> ORGANISM: Artificial Sequence
311 <220> FEATURE:
313 <223> OTHER INFORMATION: Antisense Oligonucleotide
315 <400> SEQUENCE: 11
316 tgggcccgga cccgccgcag 20
319 <210> SEQ ID NO: 12
320 <211> LENGTH: 20
321 <212> TYPE: DNA
322 <213> ORGANISM: Artificial Sequence
324 <220> FEATURE:
326 <223> OTHER INFORMATION: Antisense Oligonucleotide
328 <400> SEQUENCE: 12
329 catgggcccgc gacccgccgc 20
332 <210> SEQ ID NO: 13
333 <211> LENGTH: 20
334 <212> TYPE: DNA
335 <213> ORGANISM: Artificial Sequence
337 <220> FEATURE:
339 <223> OTHER INFORMATION: Antisense Oligonucleotide
341 <400> SEQUENCE: 13
342 ctcatgggcc cggacccgcc 20
345 <210> SEQ ID NO: 14
346 <211> LENGTH: 20
347 <212> TYPE: DNA
348 <213> ORGANISM: Artificial Sequence
350 <220> FEATURE:
352 <223> OTHER INFORMATION: Antisense Oligonucleotide
354 <400> SEQUENCE: 14
355 gcctcatggg cccggacccg 20
358 <210> SEQ ID NO: 15
359 <211> LENGTH: 20
360 <212> TYPE: DNA
361 <213> ORGANISM: Artificial Sequence
363 <220> FEATURE:
365 <223> OTHER INFORMATION: Antisense Oligonucleotide
367 <400> SEQUENCE: 15
368 tcgcctcatg ggcccggacc 20
371 <210> SEQ ID NO: 16

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VERIFICATION SUMMARY

PATENT APPLICATION: US/09/920,677

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Input Set : A:\RTS-0245 Sequence Listing.txt

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L:13 M:270 C: Current Application Number differs, Replaced Current Application No

L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date